

APPROVED	U.S. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

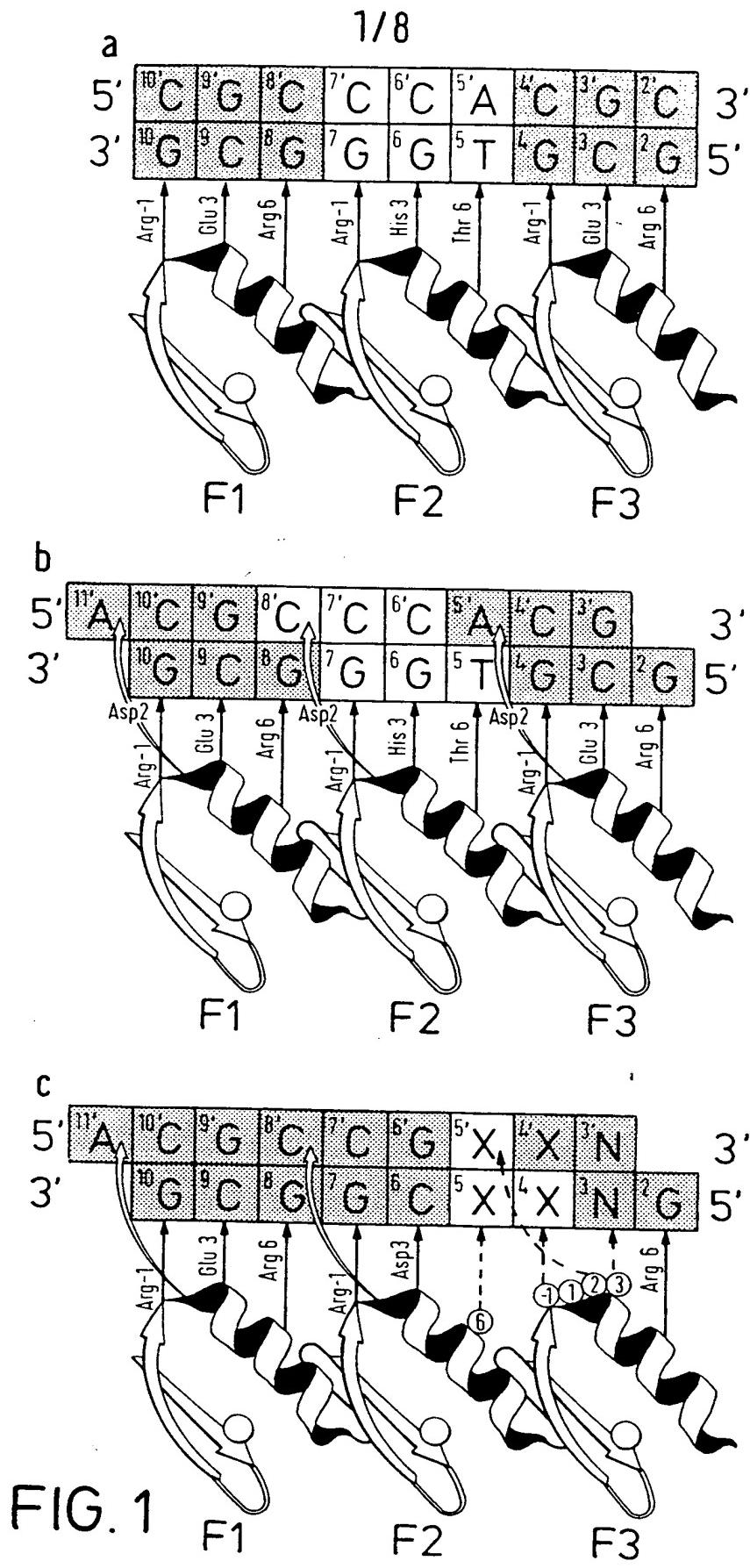


FIG. 1

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FIG. 2

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BASE AT POSITIONS ⁴ X AND ⁵ X OF DNA SITES USED IN SELECTIONS	AMINO ACIDS SELECTED IN FINGERS 2 AND 3		BINDING SITE SIGNATURE		No. OF CLONES SELECTED AND SCREENED	BASES AT POSITIONS ⁴ X AND ⁵ X OF DNA SITES USED IN SELECTIONS		AMINO ACIDS SELECTED IN FINGERS 2 AND 3		BINDING SITE SIGNATURE		No. OF CLONES SELECTED AND SCREENED				
	⁴ X ⁵ X	F2	F3	⁴ X	⁵ X	⁴ X ⁵ X	F2	F3	⁴ X	⁵ X	⁴ X ⁵ X	F2	F3	⁴ X	⁵ X	
GG	6	-1123	G A T C	G A T C	4	CC	6	-1123	G A T C	G A T C	CC	T DPHN	E HSKS	E HRQN	S DRAN	1
	R	RLEY	■■■■■	■■■■■												4
	* R	RSED	■■■■■	■■■■■												1
	R	RHTH	■■■■■	■■■■■	1											1
	R	RSSE	■■■■■	■■■■■	1											1
	R	RSSA	■■■■■	■■■■■	1											2
AG	R	QVTT	A	G	4	AC	* Y	RSQD	A	A	AC	V QVGH	T QLAT	T	A	3
	* R	QSGD	■■■■■	■■■■■	5											2
	R	QLAT	■■■■■	■■■■■	2											3
	R	QDAH	■■■■■	■■■■■	1											1
	R	QRAS	■■■■■	■■■■■	1											1
	K	QSTS	■■■■■	■■■■■	1											1
TG	R	SSGD	T	G	1	TA	N	TSQA	T	A	TA	N TSAS	K LAQT	E RSRD	E RLRD	4
	R	SASA	■■■■■	■■■■■	1											2
	* R	NSGD	■■■■■	■■■■■	1											1
	R	LVQN	■■■■■	■■■■■	1											3
	K	TGAS	■■■■■	■■■■■	1											1
	R	TPSG	■■■■■	■■■■■	1											1
	R	TQTA	■■■■■	■■■■■	1											1
	R	TSAA	■■■■■	■■■■■	2	CA	Y	HPAT	C	A	CA	N HPAN	E HHSN	L DSRA		2
CG	R	DTSV	C	G	3											1
	R	DAST	■■■■■	■■■■■	2											9
	R	DASA	■■■■■	■■■■■	1											2
	R	DTSS	■■■■■	■■■■■	2											1
GC	A	RNHD	G	C	2	GT	* T	KSSD	G	T	GT	■■■■■	■■■■■			2
	* N	RSTD	■■■■■	■■■■■	3		* K	SSSD								1
	* S	RSTD	■■■■■	■■■■■	6		* K	RSHD								1
	S	SRHS	■■■■■	■■■■■	1		A	RSSY								1
	T	RNST	■■■■■	■■■■■	1		T	RSSS								1
	T	RTST	■■■■■	■■■■■	1		T	RKTD								1
	T	TRYS	■■■■■	■■■■■	3	AT	S	QIST	A	T	AT	■■■■■	■■■■■			3
	T	RAQN	■■■■■	■■■■■	1		S	QIGA								1
AC	A	QAAT	A	C	4		T	QYST								1
	A	QGTN	■■■■■	■■■■■	1		T	QSAS								1
	* V	TSRD	■■■■■	■■■■■	4		T	QSQH ¹								1
	S	QROGA	■■■■■	■■■■■	1		T	QTSH								1
	S	QSTT	■■■■■	■■■■■	2		T	QPGH								1
	A	TSSS	■■■■■	■■■■■	1		T	QDTT								1
	T	SSST	■■■■■	■■■■■	1		K	QDST								2
TC	D	TISN	T	C	1	TT	T	TAST	T	T	TT	■■■■■	■■■■■			1
	N	TSTA	■■■■■	■■■■■	1		T	TASH								1
	V	TSSL	■■■■■	■■■■■	4		T	TSSV								1
	V	TSII	■■■■■	■■■■■	1		T	TSSA								1
	V	TSNS	■■■■■	■■■■■	3		S	HHTS								1
	* R	GSND	■■■■■	■■■■■	1		S	HAQT								1
	A	TTSS	■■■■■	■■■■■	1		S	HATT								4
	T	TAGS	■■■■■	■■■■■	1											
	S	TTSS	■■■■■	■■■■■	1											
	S	TSSA	■■■■■	■■■■■	1											
	S	LSTT	■■■■■	■■■■■	1											1
	G	LSST	■■■■■	■■■■■	1											1

RELATIVE SIGNATURE STRENGTH ■ ≤1.00 ■ 0.80 ■ 0.60 ■ 0.40 ■ 0.20 ■ 0.00

FIG. 3
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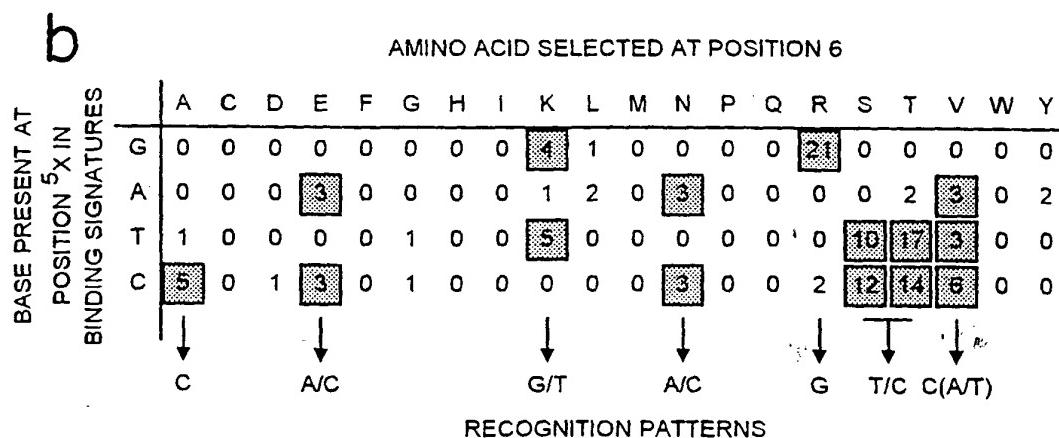
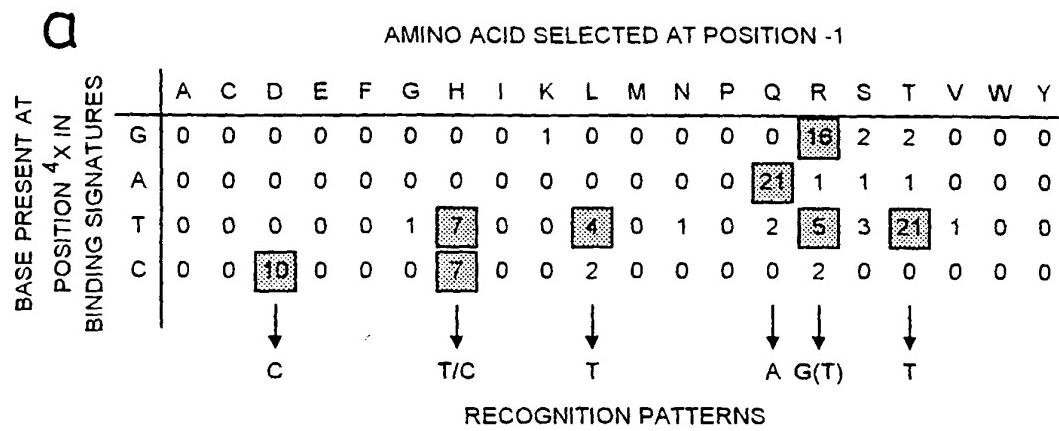
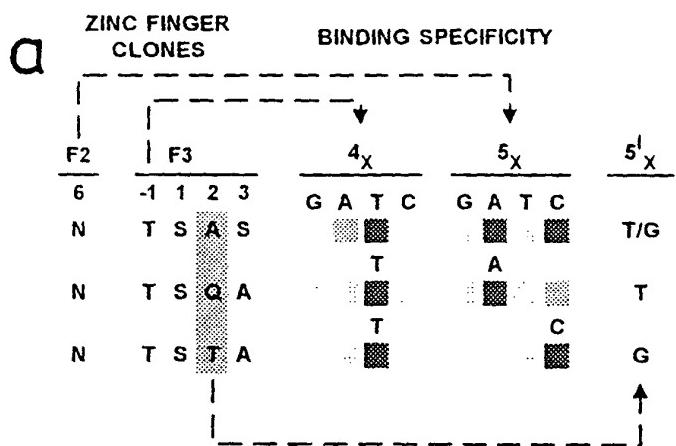


FIG. 4

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b

AMINO ACID SELECTED AT POSITION 2	ZINC FINGER CLONES				CROSS-STRAND BINDING SPECIFICITY	No. OF CLONES SELECTED AND SCREENED
	F2	F3	4 _X	5 ¹ _X		
E	R	R L E Y				4
	R	R S E D				4
N	V	T S N S				3
	R	G S N D				1
Q	Y	R S Q D				3
	Y	T S Q D				4
	K	L A Q T				1
	T	R A Q N				1
	E	H R Q N				1
	S	H A Q T				1
R	L	D S R A				2
	E	R S R D				3
	V	R L R D				4
	T	T S R D				4
H	A	R N H D				2
	S	S R H D				1
	T	D P H N				1
K	E	H S K S				4

FIG. 5

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Wild-type 5' GTG GTG GCC CCC GGC GGT GTC GGC AAG 3'
 3' CAC CAC CGG CGG CCG CCG CAC CAC CCG TTG 5'



EJ mutant 5' GTG GTG GCC CCC GTC GGT CTC GGC AAG 3'
 3' CAC CAC CGG CGG CAG CAC CAC CCG TTG 5'

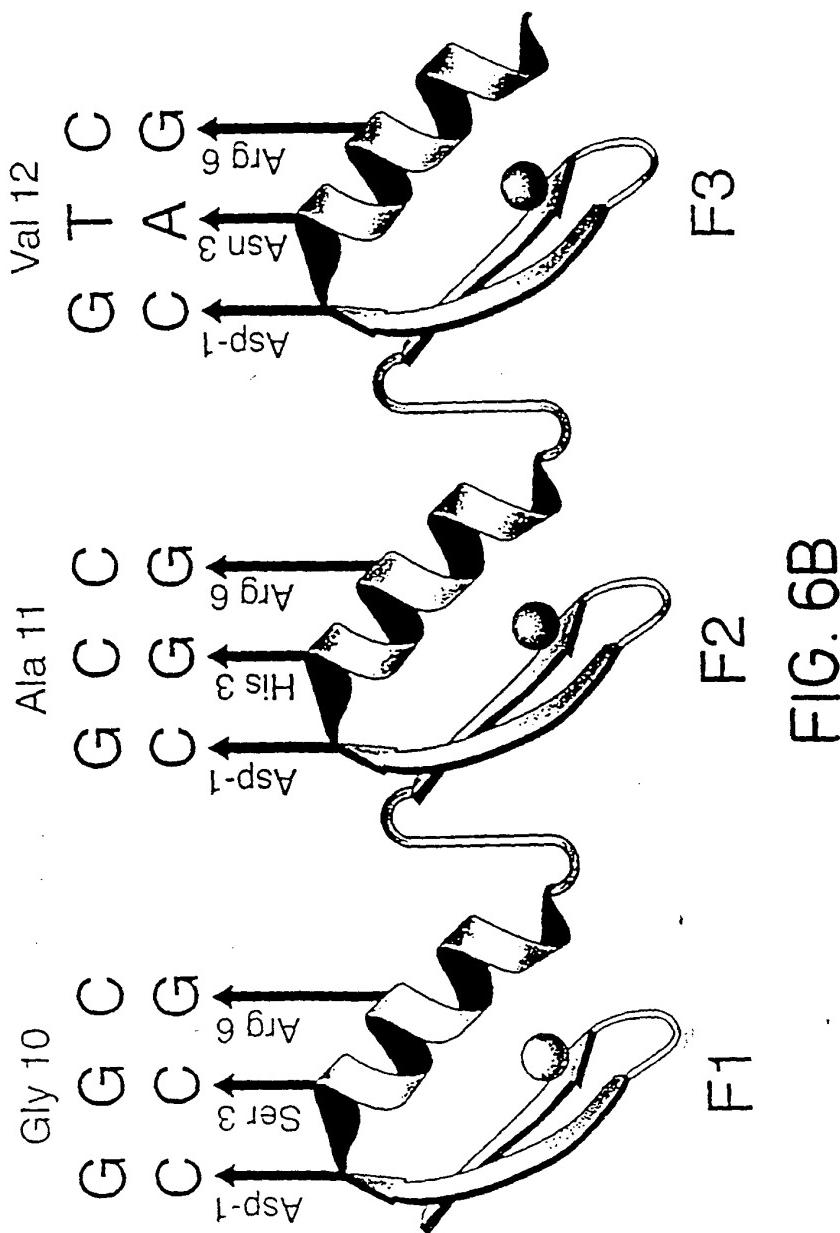
F1 M A E E' K P F~Q C R I C M R N F S D R S S L T R H T R T H T G E K P
 F2 F Q C R I C M R N F S D R S S L T R H T R T H T G E K P
 F3 F Q C R I C M R N F S D R S S L T R H T R T H T G E K P

α -helix
 β

FIG. 6C

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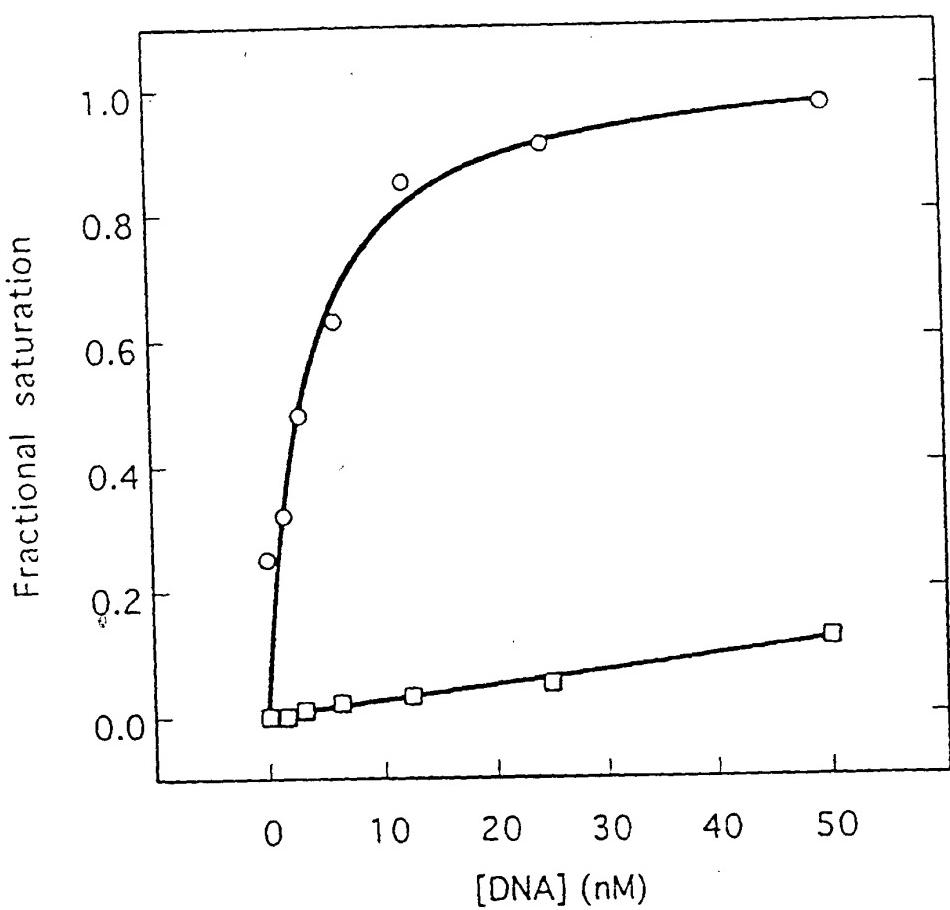


FIG. 7

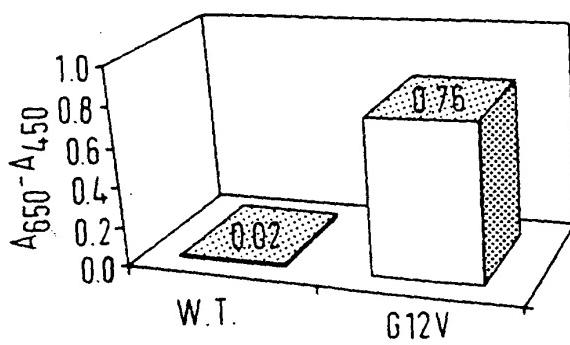


FIG. 8

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